



Culture-independent detection of *Campylobacter* by metagenomic sequencing of faecal samples

Andersen, Sandra Christine; Kiil, Kristoffer; Josefsen, Mathilde Hasseldam; Nielsen, Eva Møller; Hoorfar, Jeffrey

Publication date:
2014

Document Version
Publisher's PDF, also known as Version of record

[Link back to DTU Orbit](#)

Citation (APA):
Andersen, S. C., Kiil, K., Josefsen, M. H., Nielsen, E. M., & Hoorfar, J. (2014). *Culture-independent detection of Campylobacter by metagenomic sequencing of faecal samples*. Poster session presented at Genome Informatics 2014, Cambridge, United Kingdom.

General rights

Copyright and moral rights for the publications made accessible in the public portal are retained by the authors and/or other copyright owners and it is a condition of accessing publications that users recognise and abide by the legal requirements associated with these rights.

- Users may download and print one copy of any publication from the public portal for the purpose of private study or research.
- You may not further distribute the material or use it for any profit-making activity or commercial gain
- You may freely distribute the URL identifying the publication in the public portal

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Culture-independent detection of *Campylobacter* by metagenomic sequencing of faecal samples

Sandra Christine Andersen^{1,2} (sanan@food.dtu.dk), Kristoffer Kiil², Mathilde Hasseldam Josefsen¹, Eva Møller Nielsen², Jeffrey Hoorfar¹

¹National Food Institute, Technical University of Denmark; ²Statens Serum Institut, Denmark

Our task

- To use open-source software to detect *Campylobacter* in metagenomic datasets from sequencing of artificially inoculated faecal samples from chicken and humans
- To define a detection limit using this method
- To look at diversity among identical samples spiked with different levels of *Campylobacter*

Our conclusion

- High detection limits – 10^4 - 10^7 CFU/g
- Detection limits are lower in chicken faecal samples than in human faecal samples
- Kraken is slightly better at detection than BLAST
- Chicken faecal samples derived from same matrix and spiked with different levels of *Campylobacter* are 84-99% similar and the most abundant genera are *Lactobacillus*, *Escherichia*, and *Bacteroides*

Detection limit	BLAST	Kraken
Chicken	10^6	10^4
Human	10^7	10^6

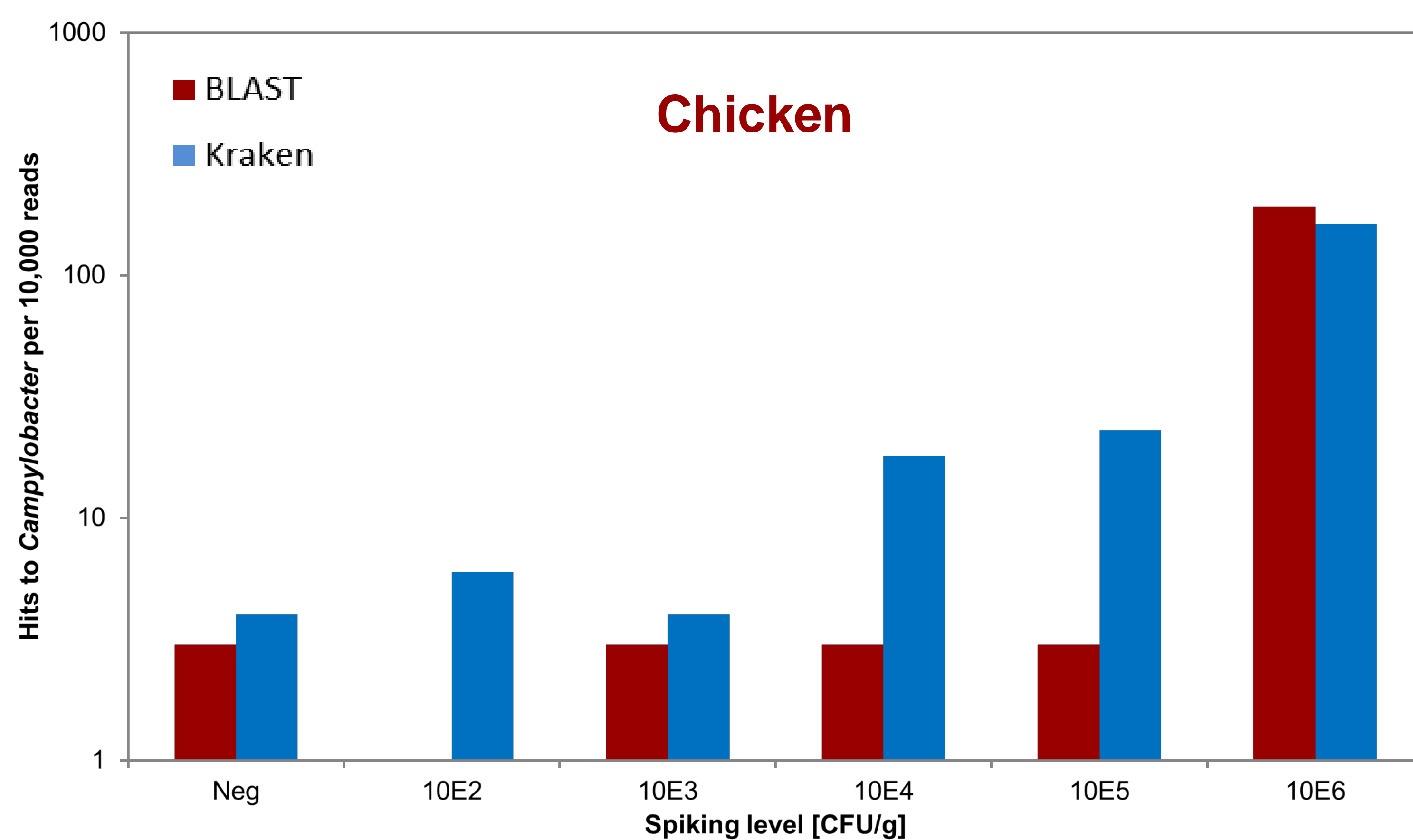


Figure 1 – Hits to *Campylobacter* found using BLAST (red) and Kraken (blue)

Detection of *Campylobacter* in chicken faecal samples is possible from 10^6 CFU/g using BLAST (red bars) and from 10^4 CFU/g using Kraken (blue bars). For BLAST results hits are number of contigs matching *Campylobacter* in proportion to the total number of contigs. For Kraken results hits are number of reads assigned to *Campylobacter* in proportion to the total number of reads.

Figure 2 – Hits to *Campylobacter* found using BLAST (red) and Kraken (blue)

Detection of *Campylobacter* in human faecal samples is possible from 10^7 CFU/g using BLAST (red bars) and from 10^6 CFU/g using Kraken (blue bars). For BLAST results hits are number of contigs matching *Campylobacter* in proportion to the total number of contigs. For Kraken results hits are number of reads assigned to *Campylobacter* in proportion to the total number of reads.

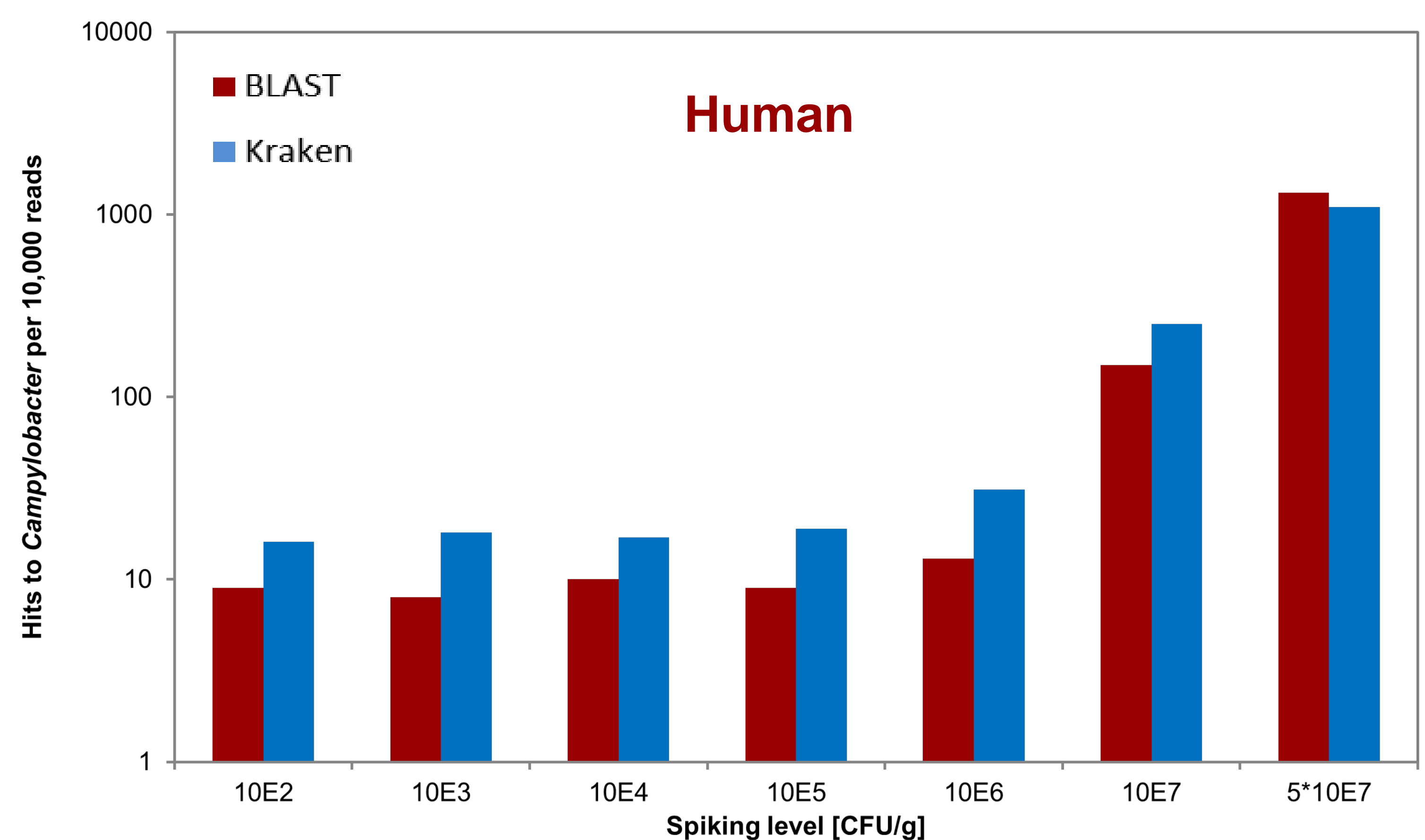


Figure 3 – Similarity in diversity

84-99% similarity is seen in diversity among the chicken faecal samples. We observe a lower similarity in the faecal sample composition than expected, since they derive from the same faecal matrix. We speculate that this is due to heterogeneity within the matrix.

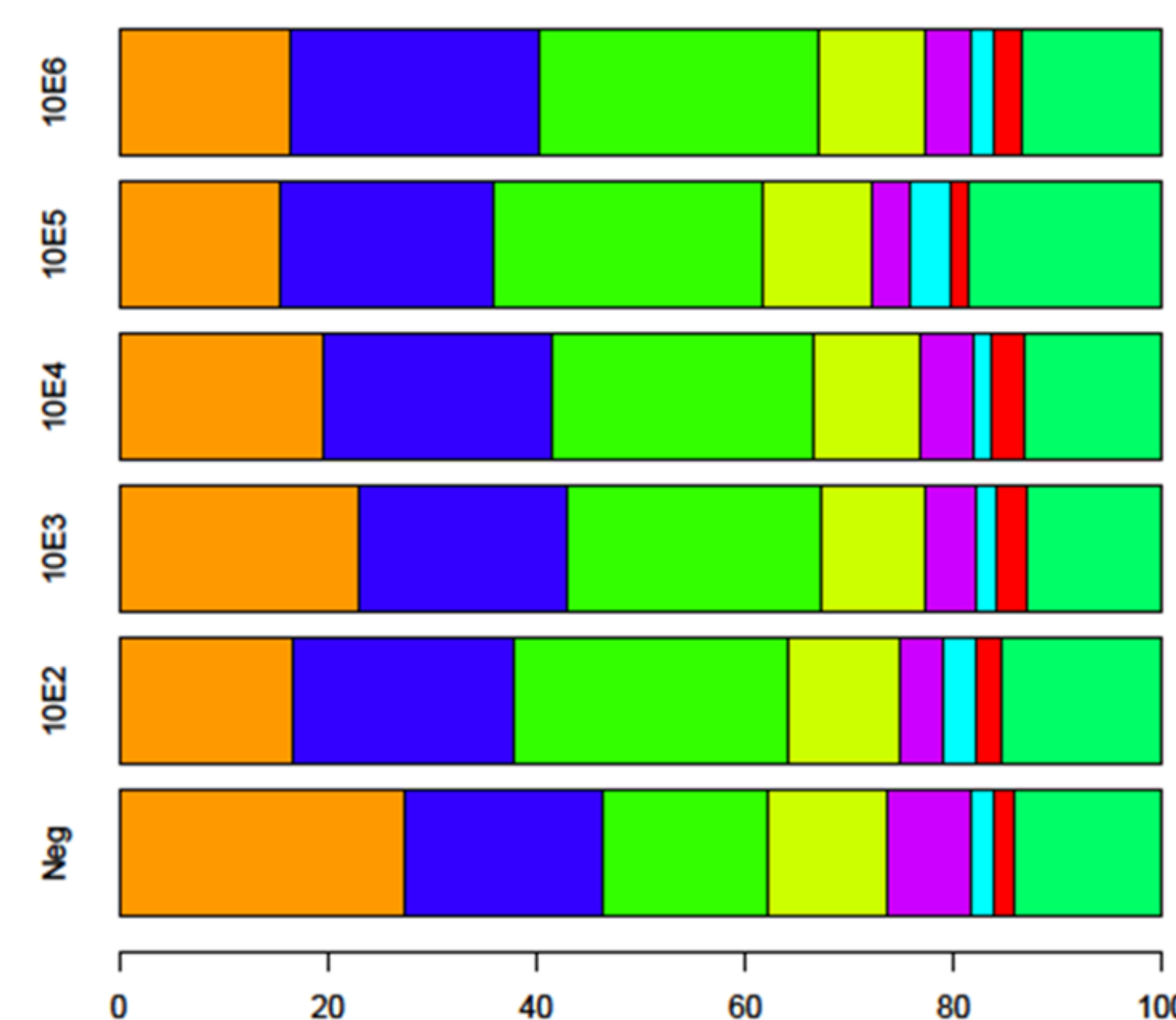
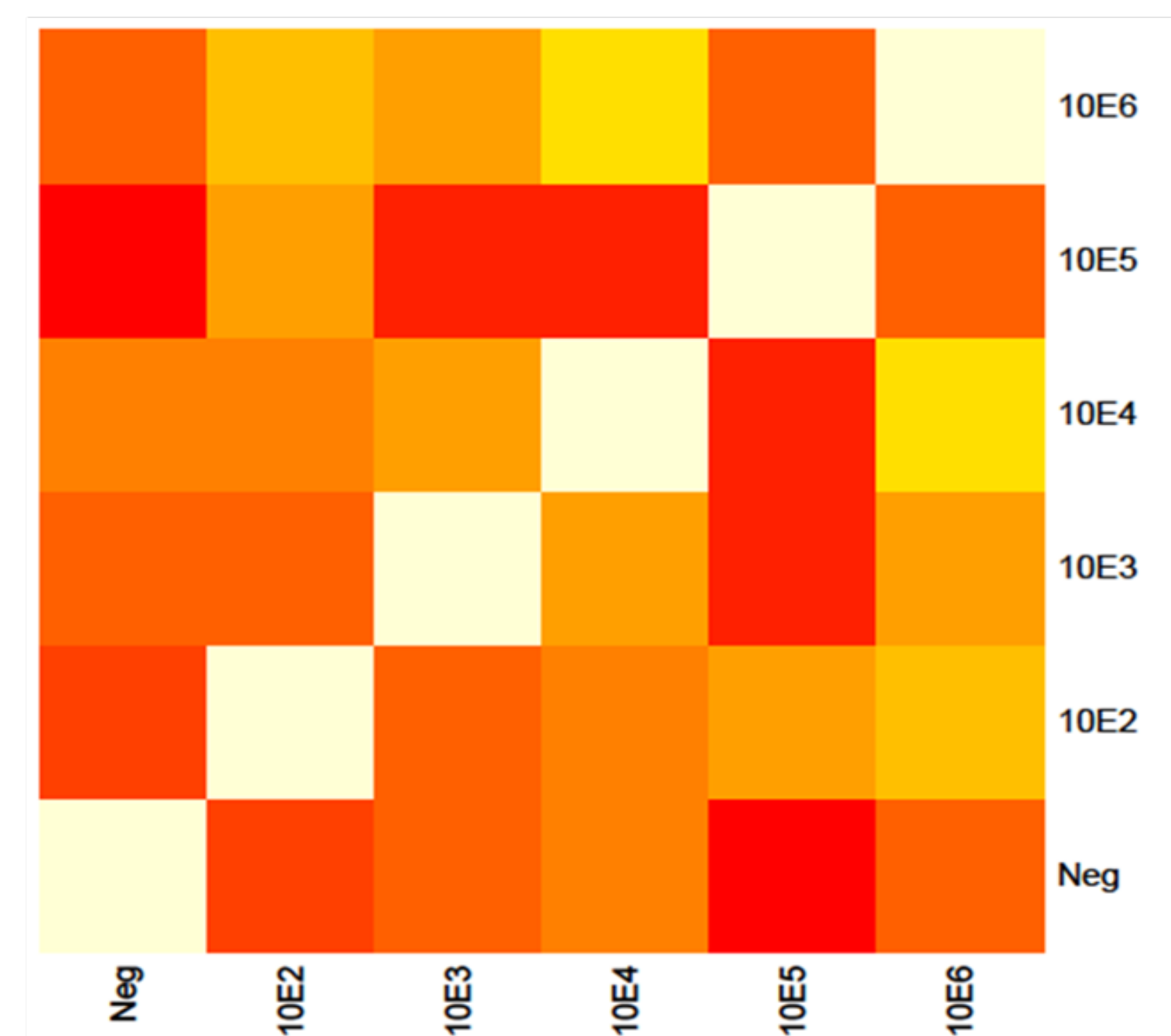


Figure 4 – Most abundant genera

Most abundant genera in the chicken faecal samples are *Lactobacillus*, *Escherichia*, and *Bacteroides*. There are more variation among the samples than we expected as they derive from same faecal matrix. Even the most abundant genus is not the same in all samples.

Next steps

- Try other software programs for detection
- Find a software solution for typing
- Look for other pathogenic bacteria
- End goal: To replace culturing and molecular analyses by diagnostic metagenomics used for detection and typing in surveillance and outbreak investigation

What we did

